



SEQUENCE LISTING

<110> Behl, Christian
Klostermann, Andreas

<120> Human semaphorin 6A-1 (SEMA6A-A), a gene involved in neuronal development and regeneration mechanisms during apoptosis, and its use as a potential drug target

<130> 48498-0100 (48498-258443)

<140> US 09/856,681
<141> 2001-08-03

<150> PCT/EP99/09215
<151> 1999-11-26

<150> EP 98122441.3
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<170> PatentIn version 3.2

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Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser	
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Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu	
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ttt gca gat gga aaa cta tac tca gcc aca gtg act gac ttc ctt gcc	1233
Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala	
180 185 190	
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Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg	
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acc gtc aag cac gat tca aaa tgg ttg aaa gaa cca tac ttt gtt caa	1329
Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln	
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gcc gtg gat tac gga gat tat atc tac ttc ttc ttc agg gaa ata gca	1377
Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala	
225 230 235 240	
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Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln	
245 250 255	
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Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln	
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Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp	
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Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg	
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Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn	
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Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala	
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Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr	
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Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys	
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Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe	
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cct gat gat acc ctg aac ttc atc aag acg cac ccg ctc atg gat gag	1857
Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu	
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Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val	
405 410 415	
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Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr	
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cag aat cac act gtg gtt ttt ctg gga tca gag aag gga atc atc ttg	2001
Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu	
435 440 445	
aag ttt ttg gcc aga ata gga aat agt ggt ttt cta aat gac agc ctt	2049
Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu	
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Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp	
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Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu	
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Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser	
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Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His	

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aat aca gat ggt ctg ggg gac tgt cac aat tcc ttt gtg gca ctg aat			2385
Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn			
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ggg cat tcc agt tcc ctc ttg ccc agc aca acc aca tca gat tcg acg			2433
Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr			
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gct caa gag ggg tat gag tct agg gga gga atg ctg gac tgg aag cat			2481
Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His			
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ctg ctt gac tca cct gac agc aca gac cct ttg ggg gca gtg tct tcc			2529
Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser			
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cat aat cac caa gac aag aag gga gtg att cgg gaa agt tac ctc aaa			2577
His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys			
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ggc cac gac cag ctg gtt ccc gtc acc ctc ttg gcc att gca gtc atc			2625
Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile			
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ctg gct ttc gtc atg ggg gcc gtc ttc tcg ggc atc acc gtc tac tgc			2673
Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys			
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gtc tgt gat cat cgg cgc aaa gac gtg gct gtg gtg cag cgc aag gag			2721
Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu			
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aag gag ctc acc cac tcg cgc cgg ggc tcc atg agc agc gtc acc aag			2769
Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys			
690	695		700
ctc agc ggc ctc ttt ggg gac act caa tcc aaa gac cca aag ccg gag			2817
Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu			
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gcc atc ctc acg cca ctc atg cac aac ggc aag ctc gcc act ccc ggc			2865
Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly			
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aac acg gcc aag atg ctc att aaa gca gac cag cac cac ctg gac ctg			2913

Asn	Thr	Ala	Lys	Met	Leu	Ile	Lys	Ala	Asp	Gln	His	His	Leu	Asp	Leu	
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Thr	Ala	Leu	Pro	Thr	Pro	Glu	Ser	Thr	Pro	Thr	Leu	Gln	Gln	Lys	Arg	
		755					760					765				
aag	ccc	agc	cgc	ggc	agc	cgc	gag	tgg	gag	agg	aac	cag	aac	ctc	atc	3009
Lys	Pro	Ser	Arg	Gly	Ser	Arg	Glu	Trp	Glu	Arg	Asn	Gln	Asn	Leu	Ile	
	770					775					780					
aat	gcc	tgc	aca	aag	gac	atg	ccc	ccc	atg	ggc	tcc	cct	gtg	att	ccc	3057
Asn	Ala	Cys	Thr	Lys	Asp	Met	Pro	Pro	Met	Gly	Ser	Pro	Val	Ile	Pro	
785					790					795					800	
acg	gac	ctg	ccc	ctg	cgg	gcc	tcc	ccc	agc	cac	atc	ccc	agc	gtg	gtg	3105
Thr	Asp	Leu	Pro	Leu	Arg	Ala	Ser	Pro	Ser	His	Ile	Pro	Ser	Val	Val	
				805					810					815		
gtc	ctg	ccc	atc	acg	cag	cag	ggc	tac	cag	cat	gag	tac	gtg	gac	cag	3153
Val	Leu	Pro	Ile	Thr	Gln	Gln	Gly	Tyr	Gln	His	Glu	Tyr	Val	Asp	Gln	
			820				825						830			
ccc	aaa	atg	agc	gag	gtg	gcc	cag	atg	gcg	ctg	gag	gac	cag	gcc	gcc	3201
Pro	Lys	Met	Ser	Glu	Val	Ala	Gln	Met	Ala	Leu	Glu	Asp	Gln	Ala	Ala	
		835					840					845				
aca	ctg	gag	tat	aag	acc	atc	aag	gaa	cat	ctc	agc	agc	aag	agt	ccc	3249
Thr	Leu	Glu	Tyr	Lys	Thr	Ile	Lys	Glu	His	Leu	Ser	Ser	Lys	Ser	Pro	
	850					855					860					
aac	cat	ggg	gtg	aac	ctt	gtg	gag	aac	ctg	gac	agc	ctg	ccc	ccc	aaa	3297
Asn	His	Gly	Val	Asn	Leu	Val	Glu	Asn	Leu	Asp	Ser	Leu	Pro	Pro	Lys	
865				870						875					880	
gtt	cca	cag	cgg	gag	gcc	tcc	ctg	ggt	ccc	ccg	gga	gcc	tcc	ctg	tct	3345
Val	Pro	Gln	Arg	Glu	Ala	Ser	Leu	Gly	Pro	Pro	Gly	Ala	Ser	Leu	Ser	
				885					890					895		
cag	acc	ggt	cta	agc	aag	cgg	ctg	gaa	atg	cac	cac	tcc	tct	tcc	tac	3393
Gln	Thr	Gly	Leu	Ser	Lys	Arg	Leu	Glu	Met	His	His	Ser	Ser	Ser	Tyr	
			900					905					910			
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Gly	Val	Asp	Tyr	Lys	Arg	Ser	Tyr	Pro	Thr	Asn	Ser	Leu	Thr	Arg	Ser	
		915					920					925				
cac	cag	gcc	acc	act	ctc	aaa	aga	aac	aac	act	aac	tcc	tcc	aat	tcc	3489
His	Gln	Ala	Thr	Thr	Leu	Lys	Arg	Asn	Asn	Thr	Asn	Ser	Ser	Asn	Ser	
		930				935					940					

tct cac ctc tcc aga aac cag agc ttt ggc agg gga gac aac ccg ccg 3537
 Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
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ccc gcc ccg cag agg gtg gac tcc atc cag gtg cac agc tcc cag cca 3585
 Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
 965 970 975

tct ggc cag gcc gtg act gtc tcg agg cag ccc agc ctc aac gcc tac 3633
 Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
 980 985 990

aac tca ctg aca agg tcg ggg ctg aag cgt acg ccc tcg cta aag ccg 3681
 Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
 995 1000 1005

gac gta ccc ccc aaa cca tcc ttt gct ccc ctt tcc aca tcc atg 3726
 Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met
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aag ccc aat gat gcg tgt aca taa tcccaggggg aggggggtcag 3770
 Lys Pro Asn Asp Ala Cys Thr
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Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
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Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
 35 40 45

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
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Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
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Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
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Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
100 105 110

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
115 120 125

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
130 135 140

Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
145 150 155 160

Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
165 170 175

Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
180 185 190

Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
195 200 205

Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
210 215 220

Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala
225 230 235 240

Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
245 250 255

Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
260 265 270

Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
 275 280 285

Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
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Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
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Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
 325 330 335

Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
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Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
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Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
 370 375 380

Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
 385 390 395 400

Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
 405 410 415

Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
 420 425 430

Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
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Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
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Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp

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Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser						
		485		490		495
Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu						
		500		505		510
Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser						
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Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His						
		530		535		540
Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly						
		545		550		555
Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn						
		565		570		575
Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr						
		580		585		590
Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His						
		595		600		605
Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser						
		610		615		620
His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys						
		625		630		635
Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile						
		645		650		655
Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys						
		660		665		670

Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu
675 680 685

Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
690 695 700

Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
705 710 715 720

Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
725 730 735

Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
740 745 750

Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg
755 760 765

Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
770 775 780

Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro
785 790 795 800

Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
805 810 815

Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
820 825 830

Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala
835 840 845

Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
850 855 860

Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
865 870 875 880

Pro Pro Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser
1 5 10 15

Gln Pro Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn
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Ala Tyr Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu
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Lys Pro Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser
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Met Lys Pro Asn Asp Ala Cys Thr
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 20 25 30

Thr Gln Pro Arg Gly Pro Leu Ser Gln Ala Pro Thr Pro Ala Pro Lys
 35 40 45

Phe Ala Pro Val Ala Pro Lys Phe Thr Pro Val Val Ser Lys Phe Ser
 50 55 60

Pro
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